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## RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/731,554

TIME: 14:28:12

Input Set : N:\Crf3\RULE60\10731554.raw

Output Set: N:\CRF4\08272004\J731554.raw

1 <110> APPLICANT: Walker, David H.  
 2 McBride, Jere W.  
 3 Yu, Xue-Jie  
 4 <120> TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein  
 5 Genes of Ehrlichia canis and Uses Thereof  
 6 <130> FILE REFERENCE: D6152CIP2  
 7 <140> CURRENT APPLICATION NUMBER: US/10/731,554  
 8 <141> CURRENT FILING DATE: 2003-12-09  
 9 <150> PRIOR APPLICATION NUMBER: US/09/811,007  
 10 <151> PRIOR FILING DATE: 2001-03-16  
 11 <150> PRIOR APPLICATION NUMBER: 09/660,587  
 12 <151> PRIOR FILING DATE: 2000-09-12  
 13 <160> NUMBER OF SEQ ID NOS: 46  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 1607  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Ehrlichia canis  
 19 <220> FEATURE:  
 20 <223> OTHER INFORMATION: nucleic acid sequence of E. canis p28-7  
 21 <400> SEQUENCE: 1  
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 23 ttttataacct aatatatata ttctggcttg tatctacttt gcacttcac tattgttaat 120  
 24 ttattttcac tatttttaggt gtaatatgaa ttgcaaaaaa attcttataa caactgcatt 180  
 25 aatatcatta atgtactcta ttccaagcat atctttttct gatactatac aagatggtaa 240  
 26 catgggtggt aacttctata ttagtggaag gtatgtacca agtgtctcac attttggtag 300  
 27 cttctcagct aaagaagaaa gcaaatcaac tgttgagggt tttggattaa aacatgattg 360  
 28 ggatggaagt ccaatactta agaataaaca cgtgacttt actgttccaa actattcgtt 420  
 29 cagatacgag aacaatccat ttctaggggt tgcaggagct atcggttact caatgggtgg 480  
 30 cccaagaata gaattcgaaa tatcttatga agcattcgac gtaaaaagtc ctaatatcaa 540  
 31 ttatcaaaat gacgcgcaca ggtactgcgc tctatctcat cacacatcg cagccatgga 600  
 32 agctgataaa tttgtcttct taaaaaacga aggggttaatt gacatatcac ttgcaataaa 660  
 33 tgcattggtat gatataataa atgacaaagt acctgtttct ccttatatat gcgcaggtat 720  
 34 tgggtactgat ttgatttcta tgtttgaagc tacaagtcct aaaatttcct accaaggaaa 780  
 35 actgggcatt agttactcta ttaatccgga aacctctgtt ttcacgggtg ggcatttcca 840  
 36 caggatcata ggtaatgagt ttagagatat tcctgcaata gtacctagta actcaactac 900  
 37 aataagtgga ccacaatttg caacagtaac actaaatgtg tgtcactttg gtttagaact 960  
 38 tggaggaaga tttaacttct aattttattg ttgccacata ttaaaaatga tctaaacttg 1020  
 39 tttttawtat tgctacatac aaaaaaagaa aaatagtggc aaaagaatgt agcaataaga 1080  
 40 gggggggggg ggaccaaatt tatcttctat gcttcccaag ttttttcygc ctatttatga 1140  
 41 cttaacaac agaaggtaat atcctcacgg aaaacttatc ttcaaatatt ttatttatta 1200  
 42 ccaatcttat ataatatatt aaatttctct tacaagaatc actagtattt tataccaaaa 1260  
 43 tatatattct gacttgcttt tcttctgcac ttctactatt ttaatttat ttgtcactat 1320  
 44 taggttataa taawatgaat tgcmaaagat ttttcatagc aagtgcattg atatcactaa 1380

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45      tgtctttctt acctagcgta tctttttctg aatcaatata tgaagataat ataaatggta 1440
46      actttttacat tagtgcaaag tatatgccaa gtgcctcaca ctttggcgta ttttcagtta 1500
47      aagaagagaa aaacacaaca actggagttt tcggattaaa acaagattgg gacggagcaa 1560
48      cactaaagga tgcaagcwg c agccacacaw tagaccaag tacaatg                1607

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50 &lt;210&gt; SEQ ID NO: 2

51 &lt;211&gt; LENGTH: 278

52 &lt;212&gt; TYPE: PRT

53 &lt;213&gt; ORGANISM: Ehrlichia canis

54 &lt;220&gt; FEATURE:

55 &lt;223&gt; OTHER INFORMATION: amino acid sequence of E. canis p28-7 protein

56 &lt;400&gt; SEQUENCE: 2

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57      Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Ile Ser Leu
58              5              10              15
59      Met Tyr Ser Ile Pro Ser Ile Ser Phe Ser Asp Thr Ile Gln Asp
60              20              25              30
61      Gly Asn Met Gly Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Val Pro
62              35              40              45
63      Ser Val Ser His Phe Gly Ser Phe Ser Ala Lys Glu Glu Ser Lys
64              50              55              60
65      Ser Thr Val Gly Val Phe Gly Leu Lys His Asp trp Asp Gly Ser
66              65              70              75
67      Pro Ile Leu Lys Asn Lys His Ala Asp Phe Thr Val Pro Asn Tyr
68              80              85              90
69      Ser Phe Arg Tyr Glu Asn Asn Pro Phe Leu Gly Phe Ala Gly Ala
70              95              100             105
71      Ile Gly Tyr Ser Met Gly Gly Pro Arg Ile Glu Phe Glu Ile Ser
72              110             115             120
73      Tyr Glu Ala Phe Asp Val Lys Ser Pro Asn Ile Asn Tyr Gln Asn
74              125             130             135
75      Asp Ala His Arg Tyr Cys Ala Leu Ser His His Thr Ser Ala Ala
76              140             145             150
77      Met Glu Ala Asp Lys Phe Val Phe Leu Lys Asn Glu Gly Leu Ile
78              155             160             165
79      Asp Ile Ser Leu Ala Ile Asn Ala Cys Tyr Asp Ile Ile Asn Asp
80              170             175             180
81      Lys Val Pro Val Ser Pro Tyr Ile Cys Ala Gly Ile Gly Thr Asp
82              185             190             195
83      Leu Ile Ser Met Phe Glu Ala Thr Ser Pro Lys Ile Ser Tyr Gln
84              200             205             210
85      Gly Lys Leu Gly Ile Ser Tyr Ser Ile Asn Pro Glu Thr Ser Val
86              215             220             225
87      Phe Ile Gly Gly His Phe His Arg Ile Ile Gly Asn Glu Phe Arg
88              230             235             240
89      Asp Ile Pro Ala Ile Val Pro Ser Asn Ser Thr Thr Ile Ser Gly
90              245             250             255
91      Pro Gln Phe Ala Thr Val Thr Leu Asn Val Cys His Phe Gly Leu
92              260             265             270
93      Glu Leu Gly Gly Arg Phe Asn Phe
94              275

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96 <210> SEQ ID NO: 3
97 <211> LENGTH: 849
98 <212> TYPE: DNA
99 <213> ORGANISM: Ehrlichia canis
100 <220> FEATURE:
101 <221> NAME/KEY: mat_peptide
102 <223> OTHER INFORMATION: nucleic acid sequence of p28-5
103 <400> SEQUENCE: 3
104   atgaattgta aaaaagtttt cacaataagt gcattgatat catccatata cttcctacct   60
105   aatgtctcat actctaacc cagtatatgg aacagtatgt atggtaattt ttacatatca  120
106   ggaaagtaca tgccaagtgt tcctcatttt ggaatttttt cagctgaaga agagaaaaaa  180
107   aagacaactg tagtatatgg cttaaaagaa aactgggcag gagatgcaat atctagtcaa  240
108   agtccagatg ataattttac cattcgaaat tactcattca agtatgcaag caacaagttt  300
109   ttaggggttg cagtagctat tggttactcg ataggcagtc caagaataga agttgagatg  360
110   tcttatgaag catttgatgt gaaaaatcca ggtgataatt acaaaaacgg tgcttacagg  420
111   tattgtgctt tatctcatca agatgatgcg gatgatgaca tgactagtgc aactgacaaa  480
112   tttgtatatt taattaatga aggattactt aacatatcat ttatgacaaa catatgttat  540
113   gaaacagcaa gcaaaaatat acctctctct cttacatat gtgcaggatg tgggtactgat  600
114   ttaattcaca tgtttgaaac tacacatcct aaaatttctt atcaaggaaa gctagggttg  660
115   gcctacttcg taagtgcaga gtcttcggtt tcttttggtt tatattttca taaaattata  720
116   aataataagt ttaaaaatgt tccagccatg gtacctatta actcagacga gatagtagga  780
117   ccacagtttg caacagtaac attaaatgta tgctactttg gattagaact tggatgtagg  840
118   ttcaacttc                                     849
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121 <211> LENGTH: 283
122 <212> TYPE: PRT
123 <213> ORGANISM: Ehrlichia canis
124 <220> FEATURE:
125 <223> OTHER INFORMATION: amino acid sequence of p28-5 protein
126 <400> SEQUENCE: 4
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129   Ile Tyr Phe Leu Pro Asn Val Ser Tyr Ser Asn Pro Val Tyr Gly
130           20                               25                30
131   Asn Ser Met Tyr Gly Asn Phe Tyr Ile Ser Gly Lys Tyr Met Pro
132           35                               40                45
133   Ser Val Pro His Phe Gly Ile Phe Ser Ala Glu Glu Glu Lys Lys
134           50                               55                60
135   Lys Thr Thr Val Val Tyr Gly Leu Lys Glu Asn Trp Ala Gly Asp
136           65                               70                75
137   Ala Ile Ser Ser Gln Ser Pro Asp Asp Asn Phe Thr Ile Arg Asn
138           80                               85                90
139   Tyr Ser Phe Lys Tyr Ala Ser Asn Lys Phe Leu Gly Phe Ala Val
140           95                               100               105
141   Ala Ile Gly Tyr Ser Ile Gly Ser Pro Arg Ile Glu Val Glu Met
142           110                              115               120
143   Ser Tyr Glu Ala Phe Asp Val Lys Asn Pro Gly Asp Asn Tyr Lys
144           125                              130               135
145   Asn Gly Ala Tyr Arg Tyr Cys Ala Leu Ser His Gln Asp Asp Ala

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146		140		145		150
147	Asp Asp Asp Met Thr Ser Ala Thr Asp Lys Phe Val Tyr Leu Ile					
148		155		160		165
149	Asn Glu Gly Leu Leu Asn Ile Ser Phe Met Thr Asn Ile Cys Tyr					
150		170		175		180
151	Glu Thr Ala Ser Lys Asn Ile Pro Leu Ser Pro Tyr Ile Cys Ala					
152		185		190		195
153	Gly Ile Gly Thr Asp Leu Ile His Met Phe Glu Thr Thr His Pro					
154		200		205		210
155	Lys Ile Ser Tyr Gln Gly Lys Leu Gly Leu Ala Tyr Phe Val Ser					
156		215		220		225
157	Ala Glu Ser Ser Val Ser Phe Gly Ile Tyr Phe His Lys Ile Ile					
158		230		235		240
159	Asn Asn Lys Phe Lys Asn Val Pro Ala Met Val Pro Ile Asn Ser					
160		245		250		255
161	Asp Glu Ile Val Gly Pro Gln Phe Ala Thr Val Thr Leu Asn Val					
162		260		265		270
163	Cys Tyr Phe Gly Leu Glu Leu Gly Cys Arg Phe Asn Phe					
164		275		280		

166 &lt;210&gt; SEQ ID NO: 5

167 &lt;211&gt; LENGTH: 840

168 &lt;212&gt; TYPE: DNA

169 &lt;213&gt; ORGANISM: Ehrlichia canis

170 &lt;220&gt; FEATURE:

171 &lt;221&gt; NAME/KEY: mat\_peptide

172 &lt;223&gt; OTHER INFORMATION: nucleic acid sequence of p28-6

173 &lt;400&gt; SEQUENCE: 5

174	atgaattgca aaaaaattct tataacaact gcattaatgt cattaatgta ctatgctcca	60
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176	aaatatgtac caagtgtttc acatttttgtt gttttctcag ctaaagaaga aagaaactca	180
177	actgttggag tttttggatt aaaacatgat tgggaatggag gtacaatata taactcttct	240
178	ccagaaaata tattcacagt tcaaaattat tcgtttaaat acgaaaacaa cccattctta	300
179	gggtttgcag gagctattgg ttattcaatg ggtggcccaa gaatagaact tgaagttctg	360
180	tacgagacat tcgatgtgaa aaatcagaac aataattata agaacggcgc acacagatac	420
181	tgtgctttat ctcatcatag ttcagcaaca agcatgtcct ccgcaagtaa caaatttggt	480
182	ttcttaaaaa atgaagggtt aattgactta tcatttatga taaatgcatg ctatgacata	540
183	ataattgaag gaatgccttt ttcaccttat atttgtgcag gtgttggtac tgatgttggt	600
184	tccatgtttg aagctataaa tcctaaaatt tcttaccaag gaaaactagg attaggttat	660
185	agtataagt cagaagcctc tgtttttatc ggtggacact ttcacagagt cataggtaat	720
186	gaatttagag acatccctgc tatggttcct agtggatcaa atcttccaga aaaccaattt	780
187	gcaatagtaa cactaaatgt gtgtcacttt ggcatagaac ttggaggaag atttaacttc	840

189 &lt;210&gt; SEQ ID NO: 6

190 &lt;211&gt; LENGTH: 280

191 &lt;212&gt; TYPE: PRT

192 &lt;213&gt; ORGANISM: Ehrlichia canis

193 &lt;220&gt; FEATURE:

194 &lt;223&gt; OTHER INFORMATION: amino acid sequence of p28-6 protein

195 &lt;400&gt; SEQUENCE: 6

196 Met Asn Cys Lys Lys Ile Leu Ile Thr Thr Ala Leu Met Ser Leu

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197		5		10		15
198	Met Tyr Tyr Ala	Pro Ser Ile Ser Phe	Ser Asp Thr Ile Gln Asp			
199		20	25	30		
200	Asp Asn Thr Gly	Ser Phe Tyr Ile Ser	Gly Lys Tyr Val Pro Ser			
201		35	40	45		
202	Val Ser His Phe	Gly Val Phe Ser Ala	Lys Glu Glu Arg Asn Ser			
203		50	55	60		
204	Thr Val Gly Val	Phe Gly Leu Lys His	Asp Trp Asn Gly Gly Thr			
205		65	70	75		
206	Ile Ser Asn Ser	Ser Pro Glu Asn Ile	Phe Thr Val Gln Asn Tyr			
207		80	85	90		
208	Ser Phe Lys Tyr	Glu Asn Asn Pro Phe	Leu Gly Phe Ala Gly Ala			
209		95	100	105		
210	Ile Gly Tyr Ser	Met Gly Gly Pro Arg	Ile Glu Leu Glu Val Leu			
211		110	115	120		
212	Tyr Glu Thr Phe	Asp Val Lys Asn Gln	Asn Asn Asn Tyr Lys Asn			
213		125	130	135		
214	Gly Ala His Arg	Tyr Cys Ala Leu Ser	His His Ser Ser Ala Thr			
215		140	145	150		
216	Ser Met Ser Ser	Ala Ser Asn Lys Phe	Val Phe Leu Lys Asn Glu			
217		155	160	165		
218	Gly Leu Ile Asp	Leu Ser Phe Met Ile	Asn Ala Cys Tyr Asp Ile			
219		170	175	180		
220	Ile Ile Glu Gly	Met Pro Phe Ser Pro	Tyr Ile Cys Ala Gly Val			
221		185	190	195		
222	Gly Thr Asp Val	Val Ser Met Phe Glu	Ala Ile Asn Pro Lys Ile			
223		200	205	210		
224	Ser Tyr Gln Gly	Lys Leu Gly Leu Gly	Tyr Ser Ile Ser Ser Glu			
225		215	220	225		
226	Ala Ser Val Phe	Ile Gly Gly His Phe	His Arg Val Ile Gly Asn			
227		230	235	240		
228	Glu Phe Arg Asp	Ile Pro Ala Met Val	Pro Ser Gly Ser Asn Leu			
229		245	250	255		
230	Pro Glu Asn Gln	Phe Ala Ile Val Thr	Leu Asn Val Cys His Phe			
231		260	265	270		
232	Gly Ile Glu Leu	Gly Gly Arg Phe Asn	Phe			
233		275	280			

235 <210> SEQ ID NO: 7  
 236 <211> LENGTH: 133  
 237 <212> TYPE: PRT  
 238 <213> ORGANISM: Ehrlichia canis  
 239 <220> FEATURE:  
 240 <223> OTHER INFORMATION: partial amino acid sequence of p28-5 protein  
 241 <400> SEQUENCE: 7

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243		5	10	15
244	Ile Tyr Phe Leu	Pro Asn Val Ser Tyr	Ser Asn Pro Val Tyr Gly	
245		20	25	30
246	Asn Ser Met Tyr	Gly Asn Phe Tyr Ile	Ser Gly Lys Tyr Met Pro	

**VERIFICATION SUMMARY**

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